

cor.estimate

0.0

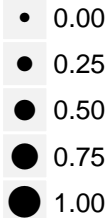
-0.1

-0.2

s2a s2b s3a s3b s4 s5 s6 s7 s8 s9 s10 s11

stage

log10(statistic + 1)



gene_set

